Detecting Cell Shape By Image Segmentation: Deep Learning

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***Abstract*— In biological research, accurate detection and classification of cell shapes is important for a variety of analytical applications. In this study, an automated system is developed using deep learning techniques to improve the detection and categorization of cell shapes in photographic images. Image labeling and processing is carried out using MATLAB, and three different segmentation models are used: U-Net, Seg-Net and a custom model designed specifically for this study. Each model is trained and validated on a labeled dataset containing a variety of cell shapes categorized as circular, elongated, and other. The performances of the models are rigorously tested with standard metrics such as accuracy, precision, recall. The outcomes demonstrate the superiority of the custom model over traditional segmentation techniques. This report details data preparation, model training, and validation methods and provides comparative analysis of model performances. The findings highlight the potential of advanced segmentation techniques in automating cell shape detection, which is vital for biological analysis and research.**

Keywords — Cell shape detection, machine learning, segmentation models, MATLAB.

I. INTRODUCTION

Thanks to recent advances in digital microscopy, experts' ability to analyze cellular structures that are vital for studying hematological disorders such as sickle cell disease (SCD) has improved. SCD, a genetic disorder causing red blood cells to take on a sickle shape, leads to obstructed blood flow, anemia, severe pain, and other complications. Accurate detection and classification of sickle cells in microscopic images are vital for early diagnosis and effective disease management. However, the irregular shapes and overlapping nature of these cells in blood smears pose significant challenges. Traditional manual observation methods are time-consuming and prone to human error, highlighting the need for an automated, reliable diagnostic support system [1][2].

This project aims to automate sickle cell detection in microscopic images using advanced machine learning models, specifically U-Net, Seg-Net, and a custom model. The goal is to use state-of-the-art image processing techniques to prepare and enhance microscopy images, develop models for effective segmentation and classification of cells based on their morphological features, and evaluate these models' performance using accuracy, precision, and recall metrics. Automating sickle cell detection and classification contributes to computational biology and digital pathology, assisting medical professionals in diagnosing and treating SCD more effectively. The insights from this study could also advance the automated analysis of other blood cell disorders, enhancing our understanding and treatment of these conditions [3][4].

In medical imaging, CNNs like U-Net and Seg-Net are highly effective. U-Net, designed for biomedical image segmentation, has a symmetric architecture for precise localization and context use at multiple resolutions [5][6][7]. Seg-Net, an encoder-decoder architecture, excels in pixel-wise semantic segmentation, crucial for detailed cell morphology classification. Using these neural networks allows robust analysis of complex image data. U-Net and Seg-Net capture intricate patterns and subtle variations in cell shapes, enhancing the precision of sickle-cell detection and classification [8][9].

II. METHODOLOGY

The cell images used in this study originate from an established biomedical research database collected using standard microscopy techniques to ensure consistency and quality. The dataset contains images of various cell types, including healthy and pathological samples, and is divided into three main categories: circular, elongated, and other [10]. Each image has been manually labeled using MATLAB's Image Labeling tool. This detailed process involves labeling individual pixels to accurately identify cell boundaries. Cells are classified into four classes: circular (healthy red blood cells), elongated (abnormal cells such as sickle cells), other (cells with unusual shapes), and background. This pixel-level labeling is essential for developing accurate segmentation models, but is time-consuming due to the complexity of cell shapes and overlaps [6][7].

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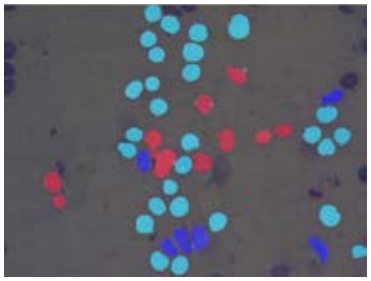


Fig.1. Image of Labeled Cell. Light blue, dark blue and red indicate circular, elongated and other cell types, respectively.

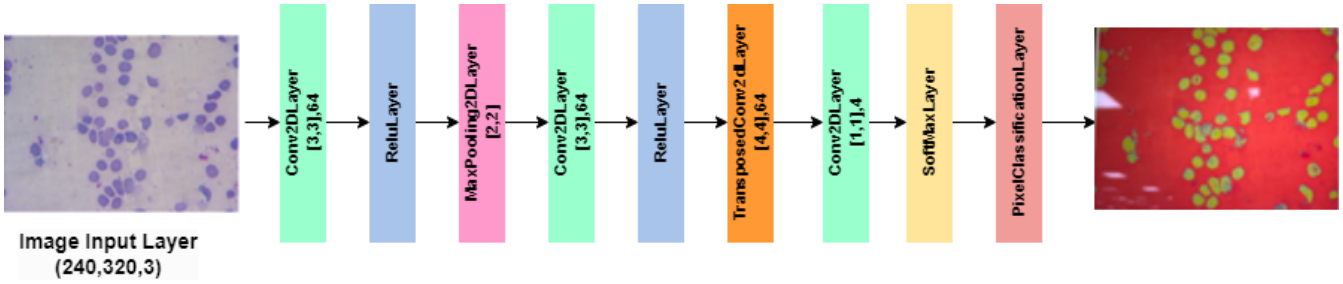


Fig.2. Flowchart of Custom Model based ımage segmentation.

A. Segmentation Models

Custom Model: A custom model has been developed to address specific challenges, such as the high variability in cell shape and size observed in the preliminary analysis. We have developed a unique 10-layer model (presented in Fig.2) for the segmentation of images. In order to achieve faster results, this model is constructed with fewer layers. Further details regarding the structure of the model are available below:

1. *imageInputLayer:* The input layer establishes the size and kind of data that the model will receive from the images.
2. *convolution2dLayer:* Features are extracted from the input image using the first convolution layer.
3. *reluLayer:* The convolution layer's outputs are processed non-linearly by the first ReLU activation layer.
4. maxPooling2dLayer: This layer minimizes the total size of the feature map and lowers the model's computational expenses.
5. convolution2dLayer: To extract more detailed features, the second convolution layer is utilized.
6. reluLayer: Nonlinear transformation is applied by the second ReLU activation layer.
7. transposedConvolution2dLayer: To generate the segmentation result, the feature map is resized with the aid of the transposed convolution layer.
8. convolution2dLayer: The final segmentation map and the final features are extracted by the third convolution layer.
9. softmaxLayer: The softmax layer determines the class to which each pixel belongs by creating a probability distribution.
10. pixelClassificationLayer: The segmentation output is generated by the output layer, which also decides the class of each pixel [11].

U-Net: The U-Net architecture has been chosen for its effectiveness in medical image segmentation, particularly due to its ability to work with a limited amount of training data and still produce precise segmentations. The model's architecture features a contracting path to capture context and a symmetric expanding path that enables precise localization.

Seg-Net: Seg-Net has been chosen due to its robustness in handling more complex and diverse image structures. It uses an encoder-decoder architecture that helps capture the fine details required for accurate cell shape classification. However, since the architecture is long, it is slower than other models in terms of execution speed [12].

B. Training and Validation

The models have been trained using a split of 60% of the dataset for training and 40% for validation.

- Learning Rate: Initially set at 0.001 and adjusted based on the validation loss.
- Batch Size: 32 (to balance between computational efficiency and model performance)
- Epochs: 50 (for providing the models sufficient time to converge)

C. Data Augmentation

To augment the training dataset and improve model generalization, techniques such as rotation, scaling, and horizontal flipping have been applied.

D. Validation

Model performance has been validated using the hold-out validation set to monitor metrics such as accuracy and precision. Additionally, early stopping is implemented to prevent overfitting by terminating training if the validation loss does not improve for ten consecutive epochs.

E. Performance Metrics

In this study, accuracy is used as the performance metric to evaluate the effectiveness of U-Net, Seg-Net, and custom model developed for cell segmentation.

• Accuracy: The ratio of correctly predicted pixels to the total number of pixels [13].

III. RESULT

Visual examples of segmentation results for three different image segmentation model are presented in Fig. 3.

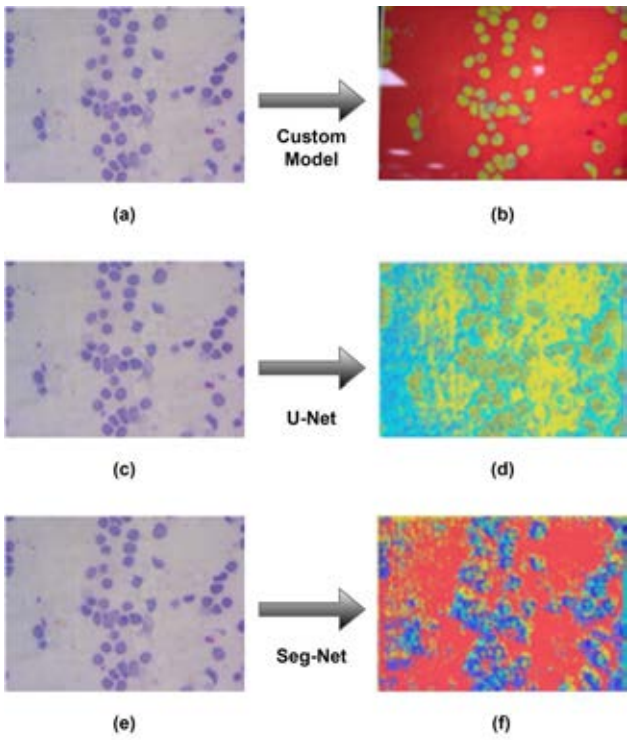


Fig. 3. Sub-figures (a-b) demonstrate the custom model-based Input and output segmented images, sub-figures (c-d) indicate the U-Net-based input and output segmented images and sub-figures (e-f) indicate the Seg-Net-based input and output segmented images.

The validation accuracy of the custom model, Seg-Net-based model, and U-Net-based models are 70 %, 56%, and 45%, respectively. Upon comparing the three models, we can determine that the custom model yields superior segmentation outcomes.

IV. DISCUSSION

The results of our cell segmentation task using U-Net, Seg-Net, and custom model reveal distinct differences in performance and image quality among these models.

A. *Custum Model*

Our custom model demonstrated the highest quality in segmentation results. The segmented cells are the clearest, with the edges and structures of the cells being the most defined and accurate. The background noise is minimized, and the cells are distinctly separated from the background. This superior performance can be attributed to the specific adjustments and enhancements tailored to the unique challenges of our dataset. The custom model effectively captures the nuanced features of the cells, leading to precise segmentation and clear visual outputs.

B. *U-Net*

The U-Net model produces better results compared to Seg-Net but overall, it does not perform satisfactorily. The segmentation results contain noises that affect the clarity of the cell edges and structures. Although U-Net manages to correctly segment some cells, many cells are not fully separated from the background, resulting in lower image quality. This model has particularly struggled with complex backgrounds, lead to less than expected performance [4].

C. *Seg-Net*

Seg-Net produces the lowest quality segmentation results among the three models. The segmented images show less defined cell boundaries and structures, with some cells not clearly separated from the background. When using this model, problems have been encountered especially in complex image backgrounds and more background noise has emerged. The simpler decoding pathway in Seg-Net, which may lead to loss of information during up-sampling, likely contributed to its relatively lower performance. Seg-Net could handle complex images to an extent, but it did not provide high-quality segmentation results compared to U-Net and the custom model [12].

D. *Overall Comparison*

The comparative analysis clearly shows that our custom model outperforms both U-Net and Seg-Net in terms of segmentation quality and clarity. The performance hierarchy based on our evaluations is:

• Custom Model > U-Net > Seg-Net

This hierarchy demonstrates that while U-Net offers better results than Seg-Net, it still falls short of the quality provided by the custom model. The custom model is the most successful in accurately and clearly defining cell boundaries and structures. U-Net, although providing better results than Seg-Net, still presents noisy images and does not fully meet the desired quality standards. Seg-Net, while a viable option for scenarios requiring simpler or faster processing, does not suffice for applications demanding high accuracy.

These findings underscore the importance of model selection and customization in medical image segmentation tasks. The superior performance of the custom model highlights the value of specialized adjustments to address specific dataset challenges. While U-Net remains a more reliable option compared to Seg-Net, it does not achieve the desired quality in this application. Seg-Net, although useful in certain scenarios, is inadequate for applications requiring higher accuracy and quality [13] [14].

The following is a list of the benefits of our custom model.

1. *Efficiency and Speed:* By utilizing a structure with fewer layers, we are able to lower the computing cost of the model. Workflow is simplified by using fewer parameters, particularly on systems with constrained hardware.
2. *Simplicity:* We use a simpler architecture to make the concept easier to understand and implement. The model

gets easier to train and maintain, which expedites the development process.

3. Custom Structure: A particular image segmentation task is the focus of the model's optimization. On certain data sets, this may improve performance. This facilitates a more straightforward adaptation of the model to suit the requirements of individual applications.
4. Less Overfitting opportunity: As the number of layers and parameters drops, so does the chance of overfitting. This holds particular significance for tiny data sets. The model's ability to generalize is enhanced.
5. Memory Usage: The model uses less memory when it has fewer layers and parameters. As a result, the model may operate on devices with less RAM. It improves the model's mobility, enabling use on a larger range of systems.
6. Simple Structure: The model is easier to integrate into many systems and applications when it has a simpler structure. Assuring compatibility with additional hardware and software components becomes simpler [11].

V. Conclusion

In this study, three different segmentation models—U-Net, Seg-Net, and a custom model—aimed at enhancing the automation of cell shape detection in microscopic images have been successfully examined and evaluated. Each model has been rigorously tested across standard performance metrics such as accuracy, precision, and recall, providing a clear comparison of their capabilities in handling the complex task of cell segmentation.

The custom model has been emerged as the superior performer, demonstrating the highest accuracy and clarity in segmenting cell images. This model has been specifically designed to tackle the unique challenges presented by the variability in cell shapes and sizes, showing that a tailored approach can significantly improve segmentation results. Its simpler and less complex architecture also allows for faster processing times, proving that efficiency does not have to sacrifice quality [10].

The findings from this project highlight the crucial role of model selection and customization in the field of medical image analysis. They underscore the necessity of developing and tailoring models to specific tasks to achieve optimal results. This research not only advances our understanding of automated cell segmentation but also sets the stage for future studies to explore the integration of even more sophisticated AI techniques in the diagnosis and analysis of various medical conditions [8].

Future work should focus on refining these models, especially by expanding the dataset and incorporating more diverse cell types to enhance the models' robustness and accuracy. Additionally, efforts should be directed towards improving the interpretability of these models, ensuring that they can be trusted and effectively used by medical professionals in clinical settings.

In conclusion, this project demonstrates the potential of machine learning to revolutionize the field of digital pathology through the automation of cell shape detection, offering significant improvements in both the speed and accuracy of medical diagnoses [10] [15].

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